SEQUENCE LISTING

<110> DING, Jeak Ling
      HO, Bow

<120> Sushi Peptide Multimer

<130> 79612-60

<140> CA2432972
<141> 2003-07-04

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<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln
 1   5   10   15

Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
              20   25   30

Leu Met

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His Ala Glu His Lys Val Lys Ile Lys Val Lys Gln Lys Tyr Gly Gln
 1   5   10   15

Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
              20   25   30

Leu Met

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TAGAAGACCC GGGGGTCCAT CAAAGAAAGT AGTTA     .    35


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                     1               5                  10

gtt cta ggg cta cta gcc caa aaa atg cgc cca gtt cag tcc aaa gga       98
Val Leu Gly Leu Leu Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly
             15                  20                  25

gta gat cta ggc ttg tgt gat gaa acg agg ttc gag tgt aag tgt ggc      146
Val Asp Leu Gly Leu Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly
             30                  35                  40

gat cca ggc tat gtg ttc aac att cca gtg aaa caa tgt aca tac ttt      194
Asp Pro Gly Tyr Val Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe
         45                  50                  55

tat cga tgg agg ccg tat tgt aaa cca tgt gat gac ctg gag gct aag      242
Tyr Arg Trp Arg Pro Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys
 60                  65                  70                  75

gat att tgt cca aag tac aaa cga tgt caa gag tgt aag gct ggt ctt      290
Asp Ile Cys Pro Lys Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu
                 80                  85                  90
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gat agt tgt gtt act tgt cca cct aac aaa tat ggt act tgg tgt agc     338
Asp Ser Cys Val Thr Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser
            95          Cys          100                 105

ggt gaa tgt cag tgt aag aat gga ggt atc tgt gac cag agg aca gga     386
Gly Glu Cys Gln Cys Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly
        110                 115                 120

gct tgt gca tgt cgt gac aga tat gaa ggg gtg cac tgt gaa att ctc     434
Ala Cys Ala Cys Arg Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu
        125             130                 135

aaa ggt tgt cct ctt ctt cca tcg gat tct cag gtt cag gaa gtc aga     482
Lys Gly Cys Pro Leu Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg
140             145                 150                 155

aat cca cca gat aat ccc caa act att gac tac agc tgt tca cca ggg     530
Asn Pro Pro Asp Asn Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly
            160                 165                 170

ttc aag ctt aag ggt atg gca cga att agc tgt ctc cca aat gga cag     578
Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln
            175                 180                 185

tgg agt aac ttt cca ccc aaa tgt att cga gaa tgt gcc atg gtt tca     626
Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser
        190                 195                 200

tct cca gaa cat ggg aaa gtg aat gct ctt agt ggt gat atg ata gaa     674
Ser Pro Glu His Gly Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu
    205                 210                 215

ggg gct act tta cgg ttc tca tgt gat agt ccc tac tac ttg att ggt     722
Gly Ala Thr Leu Arg Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly
220             225                 230                 235

caa gaa aca tta acc tgt cag ggt aat ggt cag tgg aat gga cag ata     770
Gln Glu Thr Leu Thr Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile
                240                 245                 250

cca caa tgt aag aac ttg gtc ttc tgt cct gac ctg gat cct gta aac     818
Pro Gln Cys Lys Asn Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn
        255                 260                 265

cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat ggt cag     866
His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln
        270                 275                 280

ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac tac ttc     914
Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
        285                 290                 295

ttg atg ggt ttt gac acc tta aaa tgt aac cct gat ggg tct tgg tca     962
Leu Met Gly Phe Asp Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser
300                 305                 310                 315

gga tca cag cca tcc tgt gtt aaa gtg gca gac aga gag gtc gac tgt    1010
Gly Ser Gln Pro Ser Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys
            320                 325                 330
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gac agt aaa gct gta gac ttc ttg gat gat gtt ggt gaa cct gtc agg      1058
Asp Ser Lys Ala Val Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg
            335             340             345

atc cac tgt cct gct ggc tgt tct ttg aca gct ggt act gtg tgg ggt      1106
Ile His Cys Pro Ala Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly
            350             355             360

aca gcc ata tac cat gaa ctt tcc tca gtg tgt cgt gca gcc atc cat      1154
Thr Ala Ile Tyr His Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His
            365             370             375

gct ggc aag ctt cca aac tct gga gga gcg gtg cat gtt gtg aac aat      1202
Ala Gly Lys Leu Pro Asn Ser Gly Gly Ala Val His Val Val Asn Asn
380             385             390             395

ggc ccc tac tcg gac ttt ctg ggt agt gac ctg aat ggg ata aaa tcg      1250
Gly Pro Tyr Ser Asp Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser
            400             405             410

gaa gag ttg aag tct ctt gcc cgg agt ttc cga ttc gat tat gtc cgt      1298
Glu Glu Leu Lys Ser Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg
            415             420             425

tcc tcc aca gca ggt aaa tca gga tgt cct gat gga tgg ttt gag gta      1346
Ser Ser Thr Ala Gly Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val
            430             435             440

gac gag aac tgt gtg tac gtt aca tca aaa cag aga gcc tgg gaa aga      1394
Asp Glu Asn Cys Val Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg
            445             450             455

gct caa ggt gtg tgt acc aat atg gct gct cgt ctt gct gtg ctg gac      1442
Ala Gln Gly Val Cys Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp
460             465             470             475

aaa gat gta att cca aat tcg ttg act gag act cta cga ggg aaa ggg      1490
Lys Asp Val Ile Pro Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly
            480             485             490

tta aca acc acg tgg ata gga ttg cac aga cta gat gct gag aag ccc      1538
Leu Thr Thr Thr Trp Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro
            495             500             505

ttt att tgg gag tta atg gat cgt agt aat gtg gtt ctg aat gat aac      1586
Phe Ile Trp Glu Leu Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn
            510             515             520
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cta aca ttc tgg gcc tct ggc gaa cct gga aat gaa act aac tgt gta    1634
Leu Thr Phe Trp Ala Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val
    525             530             535

tat atg gac atc caa gat cag ttg cag tct gtg tgg aaa acc aag tca    1682
Tyr Met Asp Ile Gln Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser
540             545             550             555

tgt ttt cag ccc tca agt ttt gct tgc atg atg gat ctg tca gac aga    1730
Cys Phe Gln Pro Ser Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg
                560             565             570

aat aaa gcc aaa tgc gat gat cct gga tca ctg gaa aat gga cac gcc    1778
Asn Lys Ala Lys Cys Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala
            575             580             585

aca ctt cat gga caa agt att gat ggg ttc tat gct ggt tct tct ata    1826
Thr Leu His Gly Gln Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile
            590             595             600

agg tac agc tgt gag gtt ctc cac tac ctc agt gga act gaa acc gta    1874
Arg Tyr Ser Cys Glu Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val
    605             610             615

act tgt aca aca aat ggc aca tgg agt gct cct aaa cct cga tgt atc    1922
Thr Cys Thr Thr Asn Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile
620             625             630             635

aaa gtc atc acc tgc caa aac ccc cct gta cca tca tat ggt tct gtg    1970
Lys Val Ile Thr Cys Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val
            640             645             650

gaa atc aaa ccc cca agt cgg aca aac tcg ata agt cgt gtt ggg tca    2018
Glu Ile Lys Pro Pro Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser
            655             660             665

cct ttc ttg agg ttg cca cgg tta ccc ctc cca tta gct aga gca gcc    2066
Pro Phe Leu Arg Leu Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala
            670             675             680

aaa cct cct cca aaa cct aga tcc tca caa ccc tct act gtg gac ttg    2114
Lys Pro Pro Pro Lys Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu
    685             690             695

gct tct aaa gtt aaa cta cct gaa ggt cat tac cgg gta ggg tct cga    2162
Ala Ser Lys Val Lys Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg
700             705             710             715

gcc atc tac acg tgc gag tcg aga tac tac gaa cta ctt gga tct caa    2210
Ala Ile Tyr Thr Cys Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln
                720             725             730

ggc aga aga tgt gac tct aat gga aac tgg agt ggt cgg cca gcg agc    2258
Gly Arg Arg Cys Asp Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser
                735             740             745
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tgt att cca gtt tgt gga cgg tca gac tct cct cgt tct cct ttt atc      2306
Cys Ile Pro Val Cys Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile
        750             755             760

tgg aat ggg aat tct aca gaa ata ggt cag tgg ccg tgg cag gca gga      2354
Trp Asn Gly Asn Ser Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly
    765             770             775

atc tct aga tgg ctt gca gac cac aat atg tgg ttt ctc cag tgt gga      2402
Ile Ser Arg Trp Leu Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly
780             785             790                 795

gga tct cta ttg aat gag aaa tgg atc gtc act gct gcc cac tgt gtc      2450
Gly Ser Leu Leu Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val
            800             805             810

acc tac tct gct act gct gag att att gac ccc aat cag ttt aaa atg      2498
Thr Tyr Ser Ala Thr Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met
        815             820             825

tat ctg ggc aag tac tac cgt gat gac agt aga gac gat gac tat gta      2546
Tyr Leu Gly Lys Tyr Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val
        830             835             840

caa gta aga gag gct ctt gag atc cac gtg aat cct aac tac gac ccc      2594
Gln Val Arg Glu Ala Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro
        845             850             855

ggc aat ctc aac ttt gac ata gcc cta att caa ctg aaa act cct gtt      2642
Gly Asn Leu Asn Phe Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val
860             865             870                 875

act ttg aca aca cga gtc caa cca atc tgt ctg cct act gac atc aca      2690
Thr Leu Thr Thr Arg Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr
            880             885             890

aca aga gaa cac ttg aag gag gga aca tta gca gtg gtg aca ggt tgg      2738
Thr Arg Glu His Leu Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp
        895             900             905

ggt ttg aat gaa aac aac acc tat tca gag acg att caa caa gct gtg      2786
Gly Leu Asn Glu Asn Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val
        910             915             920

cta cct gtt gtt gca gcc agc acc tgt gaa gag ggg tac aag gaa gca      2834
Leu Pro Val Val Ala Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala
        925             930             935

gac tta cca ctg aca gta aca gag aac atg ttc tgt gca ggt tac aag      2882
Asp Leu Pro Leu Thr Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys
940             945             950                 955

aag gga cgt tat gat gcc tgc agt ggg gac agt gga gga cct tta gtg      2930
Lys Gly Arg Tyr Asp Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val
            960             965             970
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ttt gct gat gat tcc cgt acc gaa agg cgg tgg gtc ttg gaa ggg att   2978
Phe Ala Asp Asp Ser Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile
        975                 980                 985

gtc agc tgg ggc agt ccc agt gga tgt ggc aag gcg aac cag tac ggg   3026
Val Ser Trp Gly Ser Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly
        990                 995                 1000

ggc ttc act aaa gtt aac gtt ttc ctg tca tgg att agg cag ttc att   3074
Gly Phe Thr Lys Val Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
   1005                 1010                 1015

tgaaactgat ctaaatattt taagcatggt tataaacgtc ttgtttccta ttattgcttt   3134

actagtttaa cccataagaa ggttaactgg gtaaggcaca aggatcattg tttctgtttg   3194

tttttacaaa tggttatttt agtcagtgaa tgagaatagt atccattgaa gactgttacc   3254

ttttattcta cctttttata ttactatgta agtatttggg atatcttcta cacatgaaaa   3314

ttctgtcatt ttaccataaa tttggtttct ggtgtgtgct aagtccacca gtagagaacg   3374

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<212> PRT
<213> Carcinoscorpius rotundicauda

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Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly Val Asp Leu Gly Leu
            20              25              30

Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly Asp Pro Gly Tyr Val
        35              40              45

Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe Tyr Arg Trp Arg Pro
     50              55              60

Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys Asp Ile Cys Pro Lys
 65              70              75              80

Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu Asp Ser Cys Val Thr
             85              90              95

Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser Gly Glu Cys Gln Cys
            100             105             110

Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly Ala Cys Ala Cys Arg
            115             120             125

Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu Lys Gly Cys Pro Leu
            130             135             140
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Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg Asn Pro Pro Asp Asn
145   150   155   160

Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly Phe Lys Leu Lys Gly
                165   170   175

Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln Trp Ser Asn Phe Pro
            180   185   190

Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser Ser Pro Glu His Gly
        195   200   205

Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu Gly Ala Thr Leu Arg
    210   215   220

Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly Gln Glu Thr Leu Thr
225   230   235   240

Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile Pro Gln Cys Lys Asn
            245   250   255

Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn His Ala Glu His Lys
            260   265   270

Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
        275   280   285

Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Gly Phe Asp
    290   295   300

Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser Gly Ser Gln Pro Ser
305   310   315   320

Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys Asp Ser Lys Ala Val
            325   330   335

Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg Ile His Cys Pro Ala
            340   345   350

Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly Thr Ala Ile Tyr His
            355   360   365

Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His Ala Gly Lys Leu Pro
    370   375   380

Asn Ser Gly Gly Ala Val His Val Val Asn Asn Gly Pro Tyr Ser Asp
385   390   395   400

Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser Glu Glu Leu Lys Ser
            405   410   415

Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg Ser Ser Thr Ala Gly
            420   425   430

Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val Asp Glu Asn Cys Val
            435   440   445

Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg Ala Gln Gly Val Cys
    450   455   460

Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp Lys Asp Val Ile Pro
465   470   475   480

Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly Leu Thr Thr Thr Trp
            485   490   495

Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro Phe Ile Trp Glu Leu
            500   505   510

Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn Leu Thr Phe Trp Ala
        515   520   525

Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val Tyr Met Asp Ile Gln
    530   535   540

Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser Cys Phe Gln Pro Ser
545   550   555   560

Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg Asn Lys Ala Lys Cys
            565   570   575

Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala Thr Leu His Gly Gln
            580   585   590

Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile Arg Tyr Ser Cys Glu
        595   600   605

Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val Thr Cys Thr Thr Asn
    610   615   620

Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile Lys Val Ile Thr Cys
625   630   635   640

Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val Glu Ile Lys Pro Pro
            645   650   655

Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser Pro Phe Leu Arg Leu
            660   665   670

Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala Lys Pro Pro Pro Lys
    675   680   685

Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu Ala Ser Lys Val Lys
    690   695   700

Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg Ala Ile Tyr Thr Cys
705   710   715   720

Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln Gly Arg Arg Cys Asp
            725   730   735

Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser Cys Ile Pro Val Cys
        740   745   750

Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile Trp Asn Gly Asn Ser
    755   760   765

Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly Ile Ser Arg Trp Leu
770   775   780

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Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly Gly Ser Leu Leu Asn
785             790             795             800

Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Thr Tyr Ser Ala Thr
            805             810             815

Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met Tyr Leu Gly Lys Tyr
        820             825             830

Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val Gln Val Arg Glu Ala
        835             840             845

Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro Gly Asn Leu Asn Phe
    850             855             860

Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val Thr Leu Thr Thr Arg
865             870             875             880

Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr Thr Arg Glu His Leu
            885             890             895

Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp Gly Leu Asn Glu Asn
            900             905             910

Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val Leu Pro Val Val Ala
        915             920             925

Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala Asp Leu Pro Leu Thr
    930             935             940

Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys Lys Gly Arg Tyr Asp
945             950             955             960

Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Phe Ala Asp Asp Ser
            965             970             975

Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile Val Ser Trp Gly Ser
        980             985             990

Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly Gly Phe Thr Lys Val
        995             1000            1005

Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
    1010            1015
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<210> 7
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> rS3-1mer

<400> 7

    Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly
    1           5               10              15
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Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr
            20                25                30

Phe Leu Met Asp
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<210> 8
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> rS3-4mer

<400> 8
ccc cag gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa     48
Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln
1                5                10                15

aaa tat ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg     96
Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
            20                25                30

ggt aac tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag    144
Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
            35                40                45

gtt aaa att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act    192
Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
    50                55                60

gaa gtg acc tat acg tgt tcg ggt aac tac ttc ttg atg gac ccc cag    240
Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
65                70                75                80

gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat    288
Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
            85                90                95

ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac    336
Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
            100                105                110

tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag gtt aaa    384
Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
            115                120                125

att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act gaa gtg    432
Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
    130                135                140

acc tat acg tgt tcg ggt aac tac ttc ttg atg gac                    468
Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
145                150                155
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<210> 9
<211> 156
<212> PRT
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<220>
<223> rS3-4mer

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Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln
1               5                   10              15

Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
            20                  25              30

Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
        35              40              45

Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
    50              55              60

Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
65              70              75              80

Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
            85              90              95

Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
            100             105             110

Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
        115             120             125

Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
    130             135             140

Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
145             150             155
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